Sequence Alignments

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: September 17, 2003, 14:04:54 ; Search time 1 Seconds
(without alignments)
6.964 Million cell updates/sec .

Title: us-09-944-896-49
Perfect score: 1876
Sequence: 1 ctcttttgtccaccagccca.........tcagctgaaaaaaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1856 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : seq264-1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1764.5	94.1	1856	1	us-09-790-264-1	
c	2	25.8	1.4	1856	1	us-09-790-264-1	

ALIGNMENTS

RESULT 1
us-09-790-264-1

Query Match 94.1%; Best Local Similarity 98.0%; Pred. No. 0;
Matches 1794; Conservative 0; Mismatches 10; Indels 27; Gaps 1;

Score 1764.5; DB 1; Length 1856;

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Qy    46 GCTCCATCCAGCCTGAGAACAAGAGCCGGGTGGCTGGCTGTGCACGGACACCTG 105
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    18 GCTCCATCCAGCCTGAGAACAAGAGCCGGGTGGCTGGCTGTGCACGGACACCTG 77

Qy   106 ACGGGCCCAACAGACCCATGGCTGCATCCAGGGTGGCTGACCCAGGGCCATCTCCTGG 165
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    78 ACGGGCCCAACAGACCCATGGCTGCATCCAGAGACTCCCCTGGGCCATCTCCTGG 137

Qy   166 CTGTGCTCCTGGCCCTCCTTGGCACCACCTGGGCACGAGGGTGTGGCCACCCAGTT 225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   138 CTGTGCTCCTGGCCCTCCTTGGCACCGCCTGACCGGCCTGGCCCACCAGTT 197

Qy   226 AGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGAGTTCTTGCTCCTCCGTGG 285
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   198 AGCAGGCTCCGATGGCCGGAGCCCTGAACAGGAAGGAGAGTTCTTGCTCCTCCGTGG 257

Qy   286 ACACACGCCTGCGCACCTGGGTCCAGCCCCCGTGGGCGGGCTGGGTCGGCTGTGCAAA 345
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   258 ACAACCGCCTGCGCAGCTGGGTCGGAGGCTTCAGCTGCCTTCAACTGGACAACCAGCGCTGCAAA 317

Qy   346 GTGACAGCAGCCTGGCCCAACTGGCTCAAGCCCAGGCAGCCCTCTGTGGAATCCCAACCCCGA 405
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   318 GTGACAGCAGCCTGGCCCAACTGGCTCAAGCCCAGGCAGCCGCCCTTGTGGAATCCCAACCCCGA 377

Qy   406 GCCTGGGCATCCGGCGCCTGGTGGCCGCCACCCTGCCAAGTGGGCTGGAGAACATCAGAGGGCAGCGGTACA 465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   378 GCCTGGGCGTCCGGCGCCTGGTGGCCGCCACCCTGCCAAGTGGGCTGGAACATCAGAGGGCAGCGGTACA 437

Qy   466 CGGGCGCTTGGGCGTCCTCTTTGTTGAAGTGGTCAGCCTATCGGTTTGCAGAGGGGGCAGCGGTGT 525
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   438 CGGGCGCTTGGGCGTCCTTTGTTGAAGTGGTCAGCCTATCGGTTTGCAGAGGGGGCAGCGGTACA 497

Qy   526 GCCACGCGGGCAGGAGGAGTGTGCTCGGAACGCCACCCACCTGCACCACTACACGGCAGCTCGTGT 585
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   498 GCCACGCGGGCAGGAGGAGTGTGCTCGGAACGCCACCCACCTGCACCACTACACGGCAGCTCGTGT 557

Qy   586 GGGCCACCTCAAGCCAGCTGGGCGTGTGGGCGGCCACCTGTGCTGCTCGCAGGACACAGGA 645
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   558 GGGCCACCTCAAGCCAGCTGGGCGTGTGGGCGGCCACCTGTGCTGCTCGCAGGACAGCAGCGA 617

Qy   646 TAGAAGCCTTTGTCTCTGCCTACTCCCCCGGAGGCGGCGGCAACTGGGAAGACAA 705
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   618 TAGAAGCCTTTGTCTCTGCCTACTCCCCCGGAGGCGGCAACTGGGAAGACAGACAA 677

Qy   706 TCATCCCCTATAGAAGAAGGGTGCCGGCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGGTGCT 765
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   678 TCATCCCCTATAGAAGAAGGGTGCCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGGTGCT 737

Qy   766 TCAAAGCCTGGGACCAATGCAGGGGGCTCTGTGAGGTGGACAGACAGGGGAATCCTTGTCCGATGA 825
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   738 TCAAAGCCTGGGACCAATGCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCCGATGA 797

Qy   826 GCTGCCAGACCATGGACGTCTCACATCAGCCACTGCCACTGCCACTGCCACTGTCCCTGGGCT 885
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   798 GCTGCCAGACCATGACGTCTCAACATCAGCCACTGCCACTGTCCCTGGGCT 857

Qy   886 ACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGCAGGGGTCCGGG 945
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   858 ACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGGGTCCGGG 917

Qy   946 AGGAGGAGTGCTTCGTTCGTTCGTTCGTGCAATCGGCTACGGGGGAGCCCCAGTGTCCACCAAGG 1005
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   918 AGGAGGAGTGCTTCGTGCGTCGTTGTGACATCGGCTACGGGGGAGCCCCAGTGTCCACCAAGG 977

Qy  1006 TGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACAGGAGGACTGCCTTCATGGTGTGTCTT 1065
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   978 TGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACAGGAGGACTGCCTTCATGGTGTCTT 1037

Qy  1066 CAGAGGCAGACCACCTATTACAGAGCCAGAGGATGAAAATGTCAGAGGAGAGAAAGGCGGGTGCTGG 1125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1038 CAGAGGCAGACACCTATTACAGAGCCAGGATGAAAATGTCAGAGGAGAAAGGCGGGGTGCTGG 1097

Qy  1126 CCCAGATCAAGAGCCAGGACCATCCTGCCCTTCTATCTGGGGCCGCCTGGGCGGGGCTGGAGA 1185
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1098 CCCAGATCAAGAGCCAGAAGTGCAGAGACATCCTGCCCTTCTATCTGGGGGCCGCCTGGGCTGGGCTGGAGA 1157

Qy  1186 CCACCAAACGAGGTGACTGACAGTGACTTCGAGACCAGGACTTCGTGGATGGGGCTCACCT 1245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1158 CCACCAAACGAGGTGATTGACAGTGACTTCGAGACCAGGAACTTCTGGATGGGGTCACCT 1217

Qy  1246 ACAAGAACCGCCAAAGGAACTCCTTCCGCCTGGGCCGCCACCAGGGCCTTCACCAGTT 1305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1218 ACAAGAACCGCCAAAGGAACTCCTTCCGCCTGGGCCACCAGGGCCTTCACCAGTT 1277

Qy  1306 TTGCCTTTGGGCAGCCTGACAACCACGGGCGTGTGGCTGAGTCGTGCCATGGGGTTGG 1365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1278 TTGCCTTTGGGCAGCCTGACAACCAC----------------------GGGTTTG 1310

Qy  1366 GCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGACAACCAGCGCTGCAAA 1425
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1311 GCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGACAACCAGCGCTGCAAA 1370
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OM protein - protein search, using sw model

Run on:           September 17, 2003, 14:00:33 ; Search time 0.001 Seconds
                                              (without alignments)
                                              202.930 Million cell updates/sec

Title:            us-09-944-896-50
Sequence:         1 MLHPETSPGRGHLLAVLLAL.........RNRYICQFAQEHISRWGPGS 455
Perfect score:    2529

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         1 seqs, 446 residues

Total number of hits satisfying chosen parameters:  1

Post-processing: Minimum Match 0%
Minimum DB seq length: 0            Maximum Match 100%
Maximum DB seq length: 200000000   Listing first 45 summaries

Database :        seq264-2:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.


                               SUMMARIES

                         %
Result       Score     Query
No.          Match Length DB  ID                              Description
-----        ----- ------ --  --                              -----------
  1          2447.5  96.8    446   1   us-09-790-264-2


                              ALIGNMENTS

RESULT 1
us-09-790-264-2

Query Match             96.8%;  Score 2447.5;  DB 1;  Length 446;
Best Local Similarity   97.1%;  Pred. No. 0;
Matches   442;  Conservative  1;  Mismatches  3;  Indels  9;  Gaps  1;

Qy      1 MLHPETSPGRGHLLAVLLALIGTTWAEVWPPQLQEQOAPMAGALNRKESFLLLSLHNRLRS 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQOAPMAGALNRKESFLLLSLHNRLRS 60

Qy     61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120

Qy    121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSOLGCGRHLCSAGQTAIEAFVC 180
          ||||||||||||||||||||||||||||||:|||||||||||||||||||| ||||||||
Db    121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSOLGCGRHLCSAGQAAIEAFVC 180

Qy    181 AYSPGGNWEVNGKIIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AYSPGGNWEVNGKIIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy    241 RLNISTCHCHCPPGYTGRRCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 RLNISTCHCHCPPGYTGRRCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300

Qy    301 TCDLRIDGSDCFMVSSEADTYYRARMKCCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCDLRIDGSDCFMVSSEADTYYRARMKCCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVI 360

Qy    361 DSDFETRNFWIGLLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWHLSAANGFGNCVEL 420
          |||||||||||||||||||||||||||||||||||||||||||||||||         ||||
Db    361 DSDFETRNFWIGLLTYKTAKDSFRWATGEHQAFTSFAFGQPDNH--------GFGNCVEL 411

Qy    421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
          ||||||||:|:|||||||||||||||||||||||
Db    412 QASAAFNWNNQRCKTRNRYICQFAQEHISRWGPGS 446


Search completed: September 17, 2003, 14:00:33
Job time : 0.001 secs
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